Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

1-89. (Canceled)

90. (Currently Amended) A method for detecting the presence or absence of a mutation characterized by the presence of a predefined nucleotide at a predefined position in a nucleic acid molecule which comprises:

(a) contacting the nucleic acid molecule with a probe comprising a first and a second nucleic acid segment, the 5' end of the first segment being covalently linked to the 3' end of the second segment, wherein either (a) the nucleotide at the 5' end of such second segment is complementary to the predefined nucleotide or (b) the nucleotide at the 3' end of such first segment is complementary to the predefined nucleotide, under conditions such that the probe hybridizes with the nucleic acid molecule;

(b) contacting the hybridized product from step (a) with a ligase under conditions such that the unlinked ends of the segments ligate together if the nucleic acid molecule contains the mutation, and

(c) determining whether the unlinked ends of the segments have ligated together, so as to thereby detect the presence or absence of the mutation in the nucleic acid molecule.

91. (Previously Presented) The method of claim 90, wherein the nucleic acid molecule is a DNA molecule.

92. (Previously Presented) The method of claim 90, wherein the nucleic acid molecule is an RNA molecule.

93. (Previously Presented) The method of claim 90, wherein the nucleic acid molecule is a mitochondrial DNA molecule.

94. (Previously Presented) The method of claim 90, wherein the nucleic acid molecule is a chromosomal DNA molecule.

95. (Previously Presented) The method of claim 90, wherein the nucleic acid molecule is a viral DNA molecule.

96. (Previously Presented) The method of claim 90, wherein the nucleic acid molecule is a cDNA molecule.

97. (Previously Presented) The method of claim 90, wherein the probe segments comprise nucleotides modified in their sugar, phosphate or base.

98. (Previously Presented) The method of claim 97, wherein the modified nucleotide is a phosphorothioate, phosphoramidate, phosphorodithioate, peptide nucleic acid, phosphonate, methylphosphonate or phosphate ester.

99. (Previously Presented) The method of claim 90, wherein the two probe segments are covalently linked by an oligonucleotide.

100. (Previously Presented) The method of claim 90, wherein the probe is labeled with a detectable moiety.

101. (Previously Presented) The method of claim 100, wherein the detectable moiety is a florescent label, a radioactive atom, a chemiluminescent label, a paramagnetic ion, biotin or a label which can be detected through a secondary enzymatic or binding step.

102. (Previously Presented) The method of claim 90, wherein the determination is by means of an enzymatic reaction selection method.

103. (Previously Presented) The method of claim 90, wherein the determination is by means of a fluorescence selection method.

104. (Previously Presented) The method of claim 90, wherein the determination is by means of a chemiluminescence selection method.

105. (Previously Presented) The method of claim 90, wherein the determination is by means of a magnetic charge selection method.

106. (Previously Presented) The method of claim 90, wherein the probe is attached to a solid support.

107. (Previously Presented) The method of claim 90, wherein the nucleic acid molecules are attached to a solid support.

108. (Previously Presented) The method of claim 90, wherein the nucleic acid molecule is circular and ligation of the unlinked ends results in catenation.

109. (Previously Presented) The method of claim 90, wherein the

mutation(s) is a point mutation.

110. (Previously Presented) The method of claim 90, wherein the mutation(s) is a deletion mutation.

111. (Previously Presented) The method of claim 90, wherein the mutation(s) is an insertion mutation.

112. (Previously Presented) The method of claim 90, wherein the mutation(s) is a translocation mutation.

113. (Previously Presented) The method of claim 90, wherein the mutation(s) is an inversion mutation.

114. (Previously Presented) The method of claim 90, wherein the nucleic acid molecule contains a plurality of detectable mutations.

115. (Currently Amended) A method for detecting the presence or absence of a predefined mutation characterized by the presence of a predefined nucleotide at a predefined position in a nucleic acid molecule associated with a genetic disorder in a subject which comprises:

(a) contacting a sample of bodily fluid or tissue from the subject containing the nucleic acid molecule associated with the genetic disorder, with a probe comprising a first and a second nucleic acid segment, the 5' end of the first segment being covalently linked to the 3' end of the second segment, wherein either (a) the nucleotide at the 5' end of such second segment is complementary to the predefined nucleotide or (b) the nucleotide at the 3' end of such first

segment is complementary to the predefined nucleotide, under conditions such that the probe hybridizes with the nucleic acid molecule~~,~~,

(b) contacting the hybridized product from step (a) with a ligase under conditions such that the unlinked ends of the segments ligate together if the nucleic acid molecule contains the predefined mutation associated with the genetic disorder, and

(c) determining whether the unlinked ends of the segments have ligated together, so as to thereby detect the presence or absence of the predefined mutation associated with the genetic disorder in the subject.

116. (Previously Presented) The method of claim 115, wherein the nucleic acid molecule(s) is covalently linked to a solid support.

117. (Previously Presented) The method of claim 115, wherein the probe(s) is covalently linked to a solid support.

118. (Currently Amended) The method of claim ~~115~~ 116 or ~~116~~ 117, wherein the solid support is a microscope slide comprised of plastic or glass, either uncoated or coated with a suitable attachment substrate.

119. (Previously Presented) The method of claim ~~115~~ 116 or ~~116~~ 117, wherein the solid support is a nylon membrane, a cellulose acetate membrane, an epoxy-activated synthetic copolymer membrane or a nitrocellulose membrane.

120. (Previously Presented) The method of claim ~~115~~ 116 or ~~116~~

117, wherein the solid support is a tube or bead or any part thereof, which is sepharose, latex, glass or plastic.

121. (Previously Presented) The method of claim 115, wherein the probe is labeled with a detectable moiety.

122. (Previously Presented) The method of claim 121, wherein the detectable moiety is a fluorescent label, a radioactive atom, a chemiluminescent label, a paramagnetic ion, biotin or a label which can be detected through a secondary enzymatic or binding step.

123. (Previously Presented) The method of claim 115, wherein the determination is by means of an enzymatic reaction selection method.

124. (Previously Presented) The method of claim 115, wherein the determination is by means of a fluorescence selection method.

125. (Previously Presented) The method of claim 115, wherein the determination is by means of a chemiluminescence selection method.

126. (Previously Presented) The method of claim 115, wherein the determination of the presence or absence of bound nucleic acid molecule(s) is by means of a magnetic charge selection method.

127. (Previously Presented) The method of claim 115, wherein the nucleic acid molecules are attached to a solid support.

128. (Previously Presented) The method of claim 115, wherein the

nucleic acid molecule is circular and ligation of the unlinked ends results in catenation.

129. (Previously Presented) The method of claim 115, wherein the genetic disorder is associated with a point mutation.

130. (Previously Presented) The method of claim 115, wherein the genetic disorder is associated with a deletion mutation.

131. (Previously Presented) The method of claim 115, wherein the genetic disorder is associated with an insertion mutation.

132. (Previously Presented) The method of claim 115, wherein the genetic disorder is associated with a translocation mutation.

133. (Previously Presented) The method of claim 115, wherein the genetic disorder is associated with an inversion mutation.

134. (Previously Presented) The method of claim 115, wherein the nucleic acid molecule contains a plurality of detectable genetic disorders.

135. (Previously Presented) A method for identifying the presence or absence of a predefined neutral polymorphism characterized by the presence of a predefined nucleotide at a predefined position in a nucleic acid molecule in a subject which comprises:

(a) contacting a sample of bodily fluid or tissue from the subject containing the nucleic acid molecule associated with the neutral polymorphism, with a probe comprising a first and a second nucleic acid segment,

the 5' end of the first segment being covalently linked to the 3' end of the second segment, wherein either (a) the nucleotide at the 5' end of such second segment is complementary to the predefined nucleotide or (b) the 3' end of such first segment is complementary to the predefined nucleotide, under conditions such that the probe hybridizes with the nucleic acid molecule;

(b) contacting the hybridized product from step (a) with a ligase under conditions such that the unlinked ends of the segments ligate together if the nucleic acid molecule contains the neutral polymorphism, and

(c) determining whether the unlinked ends of the segments have ligated together, so as to identify the presence or absence of the predefined neutral polymorphism in the subject.

136. (Previously Presented) A method for selecting a particular mutation in a nucleic acid molecule from a population of engineered nucleic acid molecules containing random mutations, which comprises:

(a) contacting a sample containing the nucleic acid molecule which may contain the particular mutation, with a probe comprising a first and a second nucleic acid segment, the 5' end of the first segment being covalently linked to the 3' end of the second segment, wherein either (a) the nucleotide at the 5' end of such second segment is complementary to the predefined nucleotide or (b) the nucleotide at the 3' end of such first segment is complementary to the predefined

nucleotide, under conditions such that the probe hybridizes with the nucleic acid molecule;

(b) contacting the hybridized product from step (a) with a ligase under conditions such that the unlinked ends of the segments ligate together if the nucleic acid molecule contains the particular mutation, and

(c) determining whether the unlinked ends of the segments have ligated together, so as to thereby select the nucleic acid molecule containing the particular mutation from the population of engineered nucleic acid molecules.

137. (Previously Presented) The method of claim 136, wherein the nucleic acid molecule is covalently linked to a solid support.

138. (Previously Presented) The method of claim 136, wherein the probe is covalently linked to a solid support.

139. (Previously Presented) The method of claim 137 or 138, wherein the solid support is a microscope slide comprised of plastic or glass.

140. (Previously Presented) The method of claim 137 or 138, wherein the solid support is a nylon or nitrocellulose membrane.

141. (Previously Presented) The method of claim 137 or 138, wherein the solid support is a bead which is sepharose, latex, glass or plastic.

142. (Previously Presented) The method of claim 136, wherein the probe is labeled with a detectable moiety.

143. (Previously Presented) The method of claim 142, wherein the detectable moiety is a florescent label, a radioactive atom, a chemiluminescent label, a paramagnetic ion, biotin or a label which can be detected through a secondary enzymatic or binding step.

144. (Previously Presented) The method of claim 136, wherein the selection is by means of an enzymatic reaction selection method.

145. (Previously Presented) The method of claim 136, wherein the selection is by means of a fluorescence based selection method.

146. (Previously Presented) The method of claim 136, wherein the selection is by means of a chemiluminescence based selection method.

147. (Previously Presented) The method of claim 136, wherein the selection is by means of magnetic charge based selection method.

148. (Previously Presented) The method of claim 136, wherein the nucleic acid molecules are attached to a solid support.

149. (Previously Presented) The method of claim 136, wherein the nucleic acid is circular and ligation of the unlinked ends results in catenation.

150. (Previously Presented) The method of claim 136, wherein the

particular mutation is associated with a point mutation.

151. (Previously Presented) The method of claim 136, wherein the particular mutation is associated with a deletion mutation.

152. (Previously Presented) The method of claim 136, wherein the particular mutation is associated with an insertion mutation.

153. (Previously Presented) The method of claim 136, wherein the particular mutation is associated with an inversion mutation.

154-161. (Canceled)

162. (Currently Amended) A method of detecting a target molecule having a defined nucleic acid sequence in a sample which comprises:

(a) providing a detectable probe with two free nucleic acid end parts which are complementary to at least a part of, and capable of hybridizing to, two regions of the target molecule, ~~and~~

(b) hybridizing the probe ends to the target molecule under hybridizing conditions[[.]],

(c) covalently connecting the ends of the hybridized probe with each other to form a circularized structure which binds the target molecule through catenation,

(d) subjecting the target molecule to denaturing conditions to release any non-circularized probe from

the target molecule, thereby retaining only the circularized probe bound to the target molecule, and

(e) detecting the presence of catenated probe, as indicative of the presence of the target molecule of defined nucleic acid sequence thus detecting the target nucleic acid in the sample.

163. (Previously Presented) A method of selectively capturing a target molecule having a defined nucleic acid sequence on a solid support which comprises:

(a) providing a probe with two free nucleic acid end parts which are complementary to at least a part of and capable of hybridizing to two regions of the target molecule, said probe being immobilized to the solid support,

(b) hybridizing the probe ends to the target molecule under hybridizing conditions,

(c) covalently connecting the ends of the hybridized probe with each other to form a circularized structure which binds with the target molecule through catenation, and

(d) subjecting the support with the capture target molecule to denaturing conditions to release any non-catenated target molecule from the support so as to selectively capture a target molecule with a defined nucleic acid sequence.